

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: SLIJKHUIS, HERMAN; SELTEN,
GERARDUS CORNELIS MARIA; SMAAL,
ERIC BASTIAAN
- (ii) TITLE OF INVENTION: PROCESS FOR OXIDATION OF
STEROIDS AND GENETICALLY ENGINEERED CELLS
USED THEREIN
- (iii) NUMBER OF SEQUENCES: 79
- (iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: BIERMAN, MUSERLIAN & LUCAS
(B) STREET: 600 THIRD AVENUE
(C) CITY: NEW YORK
(D) STATE: NEW YORK
(E) COUNTRY: USA
(F) ZIP: 10016
- (v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: FLOPPY DISK
(B) COMPUTER: IBM PC COMPATIBLE
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: MICROSOFT WORD 97
- (vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER: 09/098,990
(B) FILING DATE: 17-JUN-1998
- (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: 08/418,085
(B) FILING DATE: 06-APR-1995
- (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: 08/054,185
(B) FILING DATE: 26-APR-1993
- (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: 08/002,608
(B) FILING DATE: 11-JAN-1993
- (vii) PRIOR APPLICATION DATA:

- (A) APPLICATION NUMBER: 07/474,857
- (B) FILING DATE: 30-OCT-1990

- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: 07/474,798
 - (B) FILING DATE: 16-JULY-1990

- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: PCT/NL89/00072
 - (B) FILING DATE: 25-SEPT-1989

- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: NL88/200904.6
 - (B) FILING DATE: 06-MAY-1988

- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: NL/88/202080.3
 - (B) FILING DATE: 03-SEP-1988

- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: CHARLES A. MUSERLIAN
 - (B) REGISTRATION NUMBER: 19,683
 - (C) REFERENCE/DOCKET NUMBER: 146.1169-
CON-1-DIV-1

- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: (212) 661-8000
 - (B) TELEFAX: (212) 661-8002

(2) INFORMATION FOR SEQ ID NO: 1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 37 BASE PAIRS
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR

- (ix) FEATURE:
 - (D) OTHER INFORMATION: OLIGOMER SSC-1

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

GGCTGACGAA GTCCTGAGAC ACTGGATTCA GCACTGG

(2) INFORMATION FOR SEQ ID NO: 2:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 177 BASE PAIRS
 (B) TYPE: NUCLEIC ACID
 (C) STRANDEDNESS: DOUBLE
 (D) TOPOLOGY: LINEAR

- (ix) FEATURE:
 (D) OTHER INFORMATION: SYNTHETIC
 PSTI/HINDIII FRAGMENT

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

TGCAGCAGCG GCGGCAATCA GTACTAAGAC CCCTAGGCCT	40
TACAGTGAGA TCCCCTCCCC TGGTGACAAT GGCTGGCTTA	80
ACCTCTACCA TTTCTGGAGG GAGAAGGGCT CACAGAGAAT	120
CCACTTTCGC CACATCGAGA ACTTCCAGAA GTATGGCCCC	160
ATTTACAGGG AGAAGCT	177

(2) INFORMATION FOR SEQ ID NO: 3:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 7336 BASE PAIRS
 (B) TYPE: NUCLEIC ACID
 (C) STRANDEDNESS: DOUBLE
 (D) TOPOLOGY: UNKNOWN

- (ix) FEATURE:
 (D) OTHER INFORMATION: PLASMID pBHA-1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

AATTCACCTC GAAAGCAAGC TGATAAACCG ATACAATTAA	40
AGGCTCCTTT TGGAGCCTTT TTTTGGAG ATTTTCAACG	80
TGAAAAAATT ATTATTCGCA ATTCCAAGCT AATTCACCTC	120

GAAAGCAAGC TGATAAACCG ATACAATTAA AGGCTCCTTT	160
TGGAGCCTTT TTTTTTGGAG ATTTTCAACG TGAAAAAATT	200
ATTATTCGCA ATTCCAAGCT CTGCCTCGCG CGTTTTCGGTG	240
ATGACGGTGA AAACCTCTGA CACATGCAGC TCCCGGAGAC	280
GGTCACAGCT TGTCTGTAAG CGGATGCAGA TCACGCGCCC	320
TGTAGCGGCG CATTAAGCGC GGCGGGTGTG GTGGTTACGC	360
GCAGCGTGAC CGCTACACTT GCCAGCGCCC TAGCGCCCGC	400
TCCTTTCGCT TTCTTCCCTT CCTTTCTCGC CACGTTTCGCC	440
GGCTTTCCCC GTCAAGCTCT AAATCGGGGG CTCCCTTTAG	480
GGTTCCGATT TAGTGCTTTA CGGCACCTCG ACCCCAAAAA	520
ACTTGATTAG GGTGATGGTT CACGTAGTGG GCCATCGCCC	560
TGATAGACGG TTTTTCGCCC TTTGACGTTG GAGTCCACGT	600
TCTTTAATAG TGGACTCTTG TTCCAAACTG GAACAACACT	640
CAACCCTATC TCGGTCTATT CTTTTGATTT ATAAGGGATT	680
TTGCCGATTT CGGCCTATTG GTTAAAAAAT GAGCTGATTT	720
AACAAAAATT TAACGCGAAT TTTAACAAAA TATTAACGTT	760
TACAATTTGA TCTGCGCTCG GTCGTTTCGGC TGCGGCGAGC	800
GGTATCAGCT CACTCAAAGG CGGTAATACG GTTATCCACA	840
GAATCAGGGG ATAACGCAGG AAAGAACATG TGAGCAAAAG	880
GCCAGCAAAA GGCCAGGAAC CGTAAAAAGG CCGCGTTGCT	920
GGCGTTTTTC CATAGGCTCC GCCCCCTGA CGAGCATCAC	960
AAAAATCGAC GCTCAAGTCA GAGGTGGCGA AACCCGACAG	1000
GACTATAAAG ATACCAGGCG TTTCCCCCTG GAAGCTCCCT	1040

CGTGCGCTCT CCTGTTCCGA CCCTGCCGCT TACCGGATAC	1080
CTGTCCGCCT TTCTCCCTTC GGGAAAGCGTG GCGCTTTCTC	1120
ATAGCTCACG CTGTAGGTAT CTCAGTTCGG TGTAGGTCGT	1160
TCGCTCCAAG CTGGGCTGTG TGCACGAACC CCCC GTTCAG	1200
CCCGACCGCT GCGCCTTATC CGGTA ACTAT CGTCTTGAGT	1240
CCAACCCGGT AAGACACGAC TTATCGCCAC TGGCAGCAGC	1280
CACTGGTAAC AGGATTAGCA GAGCGAGGTA TGTAGGCGGT	1320
GCTACAGAGT TCTTGAAGTG GTGGCCTAAC TACGGCTACA	1360
CTAGAAGGAC AGTATTTGGT ATCTGCGCTC TGCTGAAGCC	1400
AGTTACCTTC GGAAAAAGAG TTGGTAGCTC TTGATCCGGC	1440
AAACAAACCA CCGCTGGTAG CGGTGGTTTT TTTGTTTGCA	1480
AGCAGCAGAT TACGCGCAGA AAAAAAGGAT CTCAAGAAGA	1520
TCCTTTGATC TTTTCTACGG GGTCTGACGC TCAGTGGAAC	1560
GAAAACTCAC GTTAAGGGAT TTTGGTCATG AGATTATCAA	1600
AAAGGATCTT CACCTAGATC CTTTTAAATT AAAAATGAAG	1640
TTTTAAATCA ATCTAAAGTA TATATGAGTA AACTTGGTCT	1680
GACAGTTACC AATGCTTAAT CAGTGAGGCA CCTATCTCAG	1720
CGATCTGTCT ATTTTCGTTCA TCCATAGTTG CCTGACTCCC	1760
CGTCGTGTAG ATAACTACGA TACGGGAGGG CTTACCATCT	1800
GGCCCCAGTG CTGCAATGAT ACCGCGAGAC CCACGCTCAC	1840
CGGCTCCAGA TTTATCAGCA ATAAACCAGC CAGCCGGAAG	1880
GGCCGAGCGC AGAAGTGGTC CTGCAACTTT ATCCGCCTCC	1920

ATCCAGTCTA	TTAATTGTTG	CCGGGAAGCT	AGAGTAAGTA	1960
GTTCGCCAGT	TAATAGTTTG	CGCAACGTTG	TTGCCATTGC	2000
TGCAGGCATC	GTGGTGTCAC	GCTCGTCGTT	TGGTATGGCT	2040
TCATTCAGCT	CCGGTTCCCA	ACGATCAAGG	CGAGTTACAT	2080
GATCCCCCAT	GTTGTGCAAA	AAAGCGGTTA	GCTCCTTCGG	2120
TCCTCCGATC	GTTGTCAGAA	GTAAGTTGGC	CGCAGTGTTA	2160
TCACTCATGG	TTATGGCAGC	ACTGCATAAT	TCTCTTACTG	2200
TCATGCCATC	CGTAAGATGC	TTTTCTGTGA	CTGGTGAGTA	2240
CTCAACCAAG	TCATTCTGAG	AATAGTGTAT	GCGGCGACCG	2280
AGTTGCTCTT	GCCCCGGCGTC	AACACGGGAT	AATACCGCGC	2320
CACATAGCAG	AACTTTAAAA	GTGCTCATCA	TTGGAAAACG	2360
TTCTTCGGGG	CGAAAACTCT	CAAGGATCTT	ACCGCTGTTG	2400
AGATCCAGTT	CGATGTAACC	CACTCGTGCA	CCCAACTGAT	2440
CTTCAGCATC	TTTTACTTTC	ACCAGCGTTT	CTGGGTGAGC	2480
AAAAACAGGA	AGGCAAAATG	CCGCAAAAAA	GGGAATAAGG	2520
GCGACACGGA	AATGTTGAAT	ACTCATACTC	TTCCTTTTTT	2560
AATATTATTG	AAGCAGACAG	TTTTATTGTT	CATGATGATA	2600
TATTTTTATC	TTGTGCAATG	TAACATCAGA	GATTTTGAGA	2640
CACAACGTGG	CTTTGTTGAA	TAAATCGAAC	TTTGCTGAG	2680
TTGACTCCCC	GCGCGCGATG	GGTCGAATTT	GCTTTCGAAA	2720
AAAAAGCCCG	CTCATTAGGC	GGGCTAAAAA	AAAGCCCGCT	2760
CATTAGGCGG	GCTCGAATTT	CTGCCATTCA	TCCGCTTATT	2800
ATCACTTATT	CAGGCGTAGC	AACCAGGCGT	TTAAGGGCAC	2840

CAATAACTGC	CTTAAAAAAA	TTACGCCCCG	CCCTGCCACT	2880
CATCGCAGTA	CTGTTGTAAT	TCATTAAGCA	TTCTGCCGAC	2920
ATGGAAGCCA	TCACAGACGG	CATGATGAAC	CTGAATCGCC	2960
AGCGGCATCA	GCACCTTGTC	GCCTTGCGTA	TAATATTTGC	3000
CCATAGTGAA	AACGGGGGCG	AAGAAGTTGT	CCATATTCGC	3040
CACGTTTAAA	TCAAACTGG	TGAAACTCAC	CCAGGGATTG	3080
GCTGAGACGA	AAAACATATT	CTCAATAAAC	CCTTTAGGGA	3120
AATAGGCCAG	GTTTTCACCG	TAACACGCCA	CATCTTGCGA	3160
ATATATGTGT	AGAAACTGCC	GGAAATCGTC	GTGGTATTCA	3200
CTCCAGAGCG	ATGAAAACGT	TTCAGTTTGC	TCATGGAAAA	3240
CGGTGTAACA	AGGGTGAACA	CTATCCCATA	TCACCAGCTC	3280
ACCGTCTTTC	ATTGCCATAC	GAAATTCGGG	ATGAGCATTC	3320
ATCAGGCGGG	CAAGAATGTG	AATAAAGGCC	GGATAAAACT	3360
TGTGCTTATT	TTTCTTTACG	GTCTTTAAAA	AGGCCGTAAT	3400
ATCCAGCTAA	ACGGTCTGGT	TATAGGTACA	TTGAGCAACT	3440
GACTGAAATG	CCTCAAAATG	TTCTTTACGA	TGCCATTGGG	3480
ATATATCAAC	GGTGGTATAT	CCAGTGATTT	TTTTCTCCAT	3520
TTTAGCTTCC	TTAGCTCCTG	AAAATCTCGA	TAActCAAAA	3560
AATACGCCCC	GTAGTGATCT	TATTTCATTA	TGGTGAAAGT	3600
TGGAACCTCT	TACGTGCCGA	TCAACGTCTC	ATTTTCGCCA	3640
AAAGTTGGCC	CAGGGCTTCC	CGGTATCAAC	AGGGACACCA	3680
GGATTTATTT	ATTCTGCGAA	GTGATCTTCC	GTCACAGGTA	3720

TTTATTCGAA	GACGAAAGGG	CATCGCGCGC	GGGGAATTCC	3760
CGGGAGAGCT	CGATATCGCA	TGCGGTACCT	CTAGAAGAAG	3800
CTTGGAGACA	AGGTAAAGGA	TAAAACAGCA	CAATTCCAAG	3840
AAAAACACGA	TTTAGAACCT	AAAAAGAACG	AATTTGAACT	3880
AACTCATAAC	CGAGAGGTAA	AAAAAGAACG	AAGTCGAGAT	3920
CAGGGAATGA	GTTTATAAAA	TAAAAAAGC	ACCTGAAAAG	3960
GTGTCTTTTT	TTGATGGTTT	TGAACTTGTT	CTTCTTATC	4000
TTGATACATA	TAGAAATAAC	GTCATTTTTA	TTTtagTTGC	4040
TGAAAGGTGC	GTTGAAGTGT	TGGTATGTAT	GTGTTTTAAA	4080
GTATTGAAAA	CCCTTAAAAT	TGGTTGCACA	GAAAAACCCC	4120
ATCTGTTAAA	GTTATAAGTG	ACTAAACAAA	TAActAAATA	4160
GATGGGGGTT	TCTTTTAATA	TTATGTGTCC	TAATAGTAGC	4200
ATTTATTCAG	ATGAAAAATC	AAGGGTTTTA	GTGGACAAGA	4240
CAAAAAGTGG	AAAAGTGAGA	CCATGGAGAG	AAAAGAAAAT	4280
CGCTAATGTT	GATTACTTTG	AACTTCTGCA	TATTCTTGAA	4320
TTTAAAAAGG	CTGAAAGAGT	AAAAGATTGT	GCTGAAATAT	4360
TAGAGTATAA	ACAAAATCGT	GAAACAGGCG	AAAGAAAGTT	4400
GTATCGAGTG	TGGTTTTGTA	AATCCAGGCT	TTGTCCAATG	4440
TGCAACTGGA	GGAGAGCAAT	GAAACATGGC	ATTCAGTCAC	4480
AAAAGGTTGT	TGCTGAAGTT	ATTAAACAAA	AGCCAACAGT	4520
TCGTTGGTTG	TTTCTCACAT	TAACAGTTAA	AAATGTTTAT	4560
GATGGCGAAG	AATTAAATAA	GAGTTTGTCA	GATATGGCTC	4600
AAGGATTTTCG	CCGAATGATG	CAATATAAAA	AAATTAATAA	4640

AAATCTTGTT	GGTTTTATGC	GTGCAACGGA	AGTGACAATA	4680
AATAATAAAG	ATAATTCTTA	TAATCAGCAC	ATGCATGTAT	4720
TGGTATGTGT	GGAACCAACT	TATTTTAAGA	ATACAGAAAA	4760
CTACGTGAAT	CAAAAACAAT	GGATTCAATT	TTGGAAAAAG	4800
GCAATGAAAT	TAGACTATGA	TCCAAATGTA	AAAGTTCAAA	4840
TGATTGACG	GAAAAATAAA	TATAAATCGG	ATATACAATC	4880
GGCAATTGAC	GAAACTGCAA	AATATCCTGT	AAAGGATACG	4920
GATTTTATGA	CCGATGATGA	AGAAAAGAAT	TTGAAACGTT	4960
TGTCTGATTT	GGAGGAAGGT	TTACACCGTA	AAAGGTTAAT	5000
CTCCTATGGT	GGTTTGTTAA	AAGAAATACA	TAAAAAATTA	5040
AACCTTGATG	ACACAGAAGA	AGGCGATTTG	ATTCATACAG	5080
ATGATGACGA	AAAAGCCGAT	GAAGATGGAT	TTTCTATTAT	5120
TGCAATGTGG	AATTGGGAAC	GGAAAAATTA	TTTTATTAAA	5160
GAGTAGTTCA	ACAAACGGGC	CAGTTTGTTG	AAGATTAGAT	5200
GCTATAATTG	TTATTAAAAG	GATTGAAGGA	TGCTTAGGAA	5240
GACGAGTTAT	TAATAGCTGA	ATAAGAACGG	TGCTCTCCAA	5280
ATATTCTTAT	TTAGAAAAGC	AAATCTAAAA	TTATCTGAAA	5320
AGGGAATGAG	AATAGTGAAT	GGACCAATAA	TAATGACTAG	5360
AGAAGAAAGA	ATGAAGATTG	TTCATGAAAT	TAAGGAACGA	5400
ATATTGGATA	AATATGGGGA	TGATGTTAAG	GCTATTGGTG	5440
TTTATGGCTC	TCTTGGTCGT	CAGACTGATG	GGCCCTATTG	5480
GGATATTGAG	ATGATGTGTG	TCATGTCAAC	AGAGGAAGCA	5520

GAGTTCAGCC ATGAATGGAC AACCGGTGAG TGGAAGGTGG	5560
AAGTGAATTT TGATAGCGAA GAGATTCTAC TAGATTATGC	5600
ATCTCAGGTG GAATCAGATT GGCCGCTTAC ACATGGTCAA	5640
TTTTTCTCTA TTTTGCCGAT TTATGATTCA GGTGGATACT	5680
TAGAGAAAGT GTATCAAACCT GCTAAATCGG TAGAAGCCCA	5720
AACGTTCCAC GATGCGATTT GTGCCCTTAT CGTAGAAGAG	5760
CTGTTTGAAT ATGCAGGCAA ATGGCGTAAT ATTCGTGTGC	5800
AAGGACCGAC AACATTTCTA CCATCCTTGA CTGTACAGGT	5840
AGCAATGGCA GGTGCCATGT TGATTGGTCT GCATCATCGC	5880
ATCTGTTATA CGACGAGCGC TTCGGTCTTA ACTGAAGCAG	5920
TTAAGCAATC AGATCTTCCT TCAGGTTATG ACCATCTGTG	5960
CCAGTTCGTA ATGTCTGGTC AACTTTCCGA CTCTGAGAAA	6000
CTTCTGGAAT CGCTAGAGAA TTTCTGGAAT GGGATTCAGG	6040
AGTGGACAGA ACGACACGGA TATATAGTGG ATGTGTCAAA	6080
ACGCATACCA TTTTGAACGA TGACCTCTAA TAATTGTTAA	6120
TCATGTTGGT TACGTATTTA TTAAGTTCTC CTAGTATTAG	6160
TAATTATCAT GGCTGTCATG GCGCATTAAAC GGAATAAAGG	6200
GTGTGCTTAA ATCGGGCCAT TTTGCGTAAT AAGAAAAAGG	6240
ATTAATTATG AGCGAATTGA ATTAATAATA AGGTAATAGA	6280
TTTACATTAG AAAATGAAAG GGGATTTTAT GCGTGAGAAT	6320
GTTACAGTCT ATCCCGGCAT TGCCAGTCGG GGATATTAAA	6360
AAGAGTATAG GTTTTTTATTG CGATAAACTA GGTTCACCTT	6400
TGGTTCACCA TGAAGATGGA TTCGCAGTTC TAATGTGTAA	6440

TGAGGTTCGG	ATTCATCTAT	GGGAGGCAAG	TGATGAAGGC	6480
TGGCGCTCTC	GTAGTAATGA	TTCACCGGTT	TGTACAGGTG	6520
CGGAGTCGTT	TATTGCTGGT	ACTGCTAGTT	GCCGCATTGA	6560
AGTAGAGGGA	ATTGATGAAT	TATATCAACA	TATTAAGCCT	6600
TTGGGCATTT	TGCACCCCAA	TACATCATTA	AAAGATCAGT	6640
GGTGGGATGA	ACGAGACTTT	GCAGTAATTG	ATCCCGACAA	6680
CAATTTGATT	AGCTTTTTTC	AACAAATAAA	AAGCTAAAAT	6720
CTATTATTAA	TCTGTTTCAGC	AATCGGGCGC	GATTGCTGAA	6760
TAAAAGATAC	GAGAGACCTC	TCTTGTATCT	TTTTTATTTT	6800
GAGTGGTTTT	GTCCGTTACA	CTAGAAAACC	GAAAGACAAT	6840
AAAAATTTTA	TTCTTGCTGA	GTCTGGCTTT	CGGTAAGCTA	6880
GACAAAACGG	ACAAAATAAA	AATTGGCAAG	GGTTTAAAGG	6920
TGGAGATTTT	TTGAGTGATC	TTCTCAAAAA	ATACTACCTG	6960
TCCCTTGCTG	ATTTTTTAAAC	GAGCACGAGA	GCAAAACCCC	7000
CCTTTGCTGA	GGTGGCAGAG	GGCAGGTTTT	TTTGTTTCTT	7040
TTTTCTCGTA	AAAAAAAGAA	AGGTCTTAAA	GGTTTTATGG	7080
TTTTGGTCGG	CACTGCCGAC	AGCCTCGCAG	GACACACACT	7120
TTATGAATAT	AAAGTATAGT	GTGTTATACT	TTACTTGGA	7160
GTGGTTGCCG	GAAAGAGCGA	AAATGCCTCA	CATTTGTGCC	7200
ACCTAAAAAG	GAGCGATTTA	CATATGAGTT	ATGCAGTTTG	7240
TAGAATGCAA	AAAGTGAAAT	CAGGGGGATC	CTCTAGAGTC	7280
GAGCTCAAGC	TAGCTTGGTA	CGTACCAGAT	CTGAGATCAC	7320

GCGTTCTAGA GGTCGA

7336

(2) INFORMATION FOR SEQ ID NO: 4:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 27 BASE PAIRS
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: UNKNOWN

- (ix) FEATURE:
(D) OTHER INFORMATION: SPHI/STUI FRAGMENT
IN pGBSCC-4

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

CATATGATCA GTACTAAGAC CCCTAGG

27

(2) INFORMATION FOR SEQ ID NO: 5:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 31 BASE PAIRS
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: UNKNOWN

- (ix) FEATURE:
(D) OTHER INFORMATION: SPHI/STUI FRAGMENT
IN pGBSCC-4

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

CCTAGGGGTC TTAGTACTGA TCATATGCAT G

31

(2) INFORMATION FOR SEQ ID NO: 6:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 41 BASE PAIRS
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: UNKNOWN

(ix) FEATURE:
(D) OTHER INFORMATION: SPHI/STUI FRAGMENT
IN pGBSSC-3, FIGURE 7

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

CTGCAGCAGC GGCGGCAATC AGTACTAAGA CCCCTAGGCC T 41

(2) INFORMATION FOR SEQ ID NO: 7:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 BASE PAIRS
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: LINEAR

(ix) FEATURE:
(D) OTHER INFORMATION: NDEI RESTRICTION
SITE AT THE ATG INITIATION CODON OF
THE LACZ GENE IN PTZ18R

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

CAGGAAACAC ATATGACCAT GATT 24

(2) INFORMATION FOR SEQ ID NO: 8:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 108 BASE PAIRS
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: UNKNOWN

(ix) FEATURE:
(D) OTHER INFORMATION: LACTASE TERMINATOR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

TCGACGCGGC CGCAGATCTG ATATCTCGAG AATTTATACT 40

TAGATAAGTA TGTACTTACA GGTATATTTC TATGAGATAC 80

TGATGTATAC ATGCATGATA ATATTTAA 108

(2) INFORMATION FOR SEQ ID NO: 9:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 44 BASE PAIRS
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: UNKNOWN

- (ix) FEATURE:
(D) OTHER INFORMATION: SALI/XHOI FRAGMENT
IN pGBSCC-6

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

TCGACAAAAA TGATCAGTAC TAAGACTCCT AGGCCTATCG ATTC 44

(2) INFORMATION FOR SEQ ID NO: 10:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 44 BASE PAIRS
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: UNKNOWN

- (ix) FEATURE:
(D) OTHER INFORMATION: SALI/XHOI FRAGMENT
IN pGBSCC-6

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

TCGAGAATCG ATAGGCCTAG GAGTCTTAGT ACTGATCATT TTTG 44

(2) INFORMATION FOR SEQ ID NO: 11:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 158 BASE PAIRS
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: UNKNOWN

- (ix) FEATURE:

(D) OTHER INFORMATION: SALI/XHOI
SYNTHETIC DNA IN PLASMID pGBSCC-11

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

TCGACAAAAA TGTTGGCTCG AGGTTTGCCA TTGAGATCCG	40
CTTTGGTTAA GGCTTGTCCA CCAATCTTGT CCACTGTTGG	80
TGAAGGTTGG GGTCACCACA GAGTTGGTAC TGGTGAAGGT	120
GCTGGTATCA GTACTAAGAC TCCTAGGCCT ATCGATTC	158

(2) INFORMATION FOR SEQ ID NO: 12:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 158 BASE PAIRS
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: UNKNOWN

(ix) FEATURE:
(D) OTHER INFORMATION: SALI/XHOI
SYNTHETIC DNA IN PLASMID pGBSCC-11

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

TCGAGAATCG ATAGGCCTAG GAGTCTTAGT ACTGATACCA	40
GCACCTTCAC CAGTACCAAC TCTGTGGTGA CCCCAACCTT	80
CACCAACAGT GGACAAGATT GGTGGACAAG CCTTAACCAA	120
AGCGGATCTC AATGGCAAAC CTCGAGCCAA CATTTTTG	158

(2) INFORMATION FOR SEQ ID NO: 13:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 161 BASE PAIRS
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: UNKNOWN

(ix) FEATURE:
(D) OTHER INFORMATION: SALI/XHOI
SYNTHETIC DNA IN pGBSSC-14

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

TCGACAAAAA TGTTGTCTCG AGCTATCTTC AGAAACCCAG	40
TTATCAACAG AACTTTGTTG AGAGCTAGAC CAGGTGCTTA	80
CCACGCTACT AGATTGACTA AGAACACTTT CATCCAATCC	120
AGAAAGTACA TCAGTACTAA GACTCCTAGG CCTATCGATT	160
C	161

(2) INFORMATION FOR SEQ ID NO: 14:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 161 BASE PAIRS
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: UNKNOWN

(ix) FEATURE:
(D) OTHER INFORMATION: SALI/XHOI
SYNTHETIC DNA IN pGBSCC-14

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

TCGAGAATCG ATAGGCCTAG GAGTCTTAGT ACTGATGTAC	40
TTTCTGGATT GGATGAAAGT GTTCTTAGTC AATCTAGTAG	80
CGTGGTAAGC ACCTGCTCTA GCTCTCAACA AAGTTCTGTT	120
GATAACTGGG TTTCTGAAGA TAGCTCGAGA CAACATTTTT	160
G	161

(2) INFORMATION FOR SEQ ID NO: 15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 BASE PAIRS
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

- (ix) FEATURE:
 - (D) OTHER INFORMATION: OLIGOMER 17
ALPHA-1

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

AGTGGCCACT TTGGGACGCC CAGAGAATTC

30

(2) INFORMATION FOR SEQ ID NO: 16:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 36 BASE PAIRS
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: DOUBLE
 - (D) TOPOLOGY: LINEAR

- (ix) FEATURE:
 - (D) OTHER INFORMATION: OLIGOMER 17
ALPHA-2

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

GAGGCTCCTG GGGTACTTGG CACCAGAGTG CTTGGT

36

(2) INFORMATION FOR SEQ ID NO: 17:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 43 BASE PAIRS
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR

- (ix) FEATURE:
 - (D) OTHER INFORMATION: SEQUENCE OF pGB17
ALPHA-3 MUTATED BY SITE DIRECTED
MUTAGENESIS, FIGURE 23

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:

TCTTTGTCCT GACTGCTGCC ACCCAGACAC AATGTGGCTG CTC

43

(2) INFORMATION FOR SEQ ID NO: 18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 43 BASE PAIRS
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: SINGLE
- (D) TOPOLOGY: LINEAR

(ix) FEATURE:

- (D) OTHER INFORMATION: SYNTHETIC OLIGOMER
17 ALPHA-3 WITH SALI SITE

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:

TCTTTGTCCT GACTGCTGCC AGTCGACAAA AATGTGGCTG CTC

43

(2) INFORMATION FOR SEQ ID NO: 19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 BASE PAIRS
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ix) FEATURE:

- (D) OTHER INFORMATION: SEQUENCE OF pGB17
ALPHA-3 MUTATED BY SITE DIRECTED
MUTAGENESIS TO CREATE A NDEI SITE,
FIGURE 25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:

GCTGCCACCC AGACACAATG TGGCTGCTCC T

31

(2) INFORMATION FOR SEQ ID NO: 20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 BASE PAIRS
- (B) TYPE: NUCLEIC ACID

(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ix) FEATURE:
(D) OTHER INFORMATION: SYNTHETIC OLIGOMER
17 ALPHA-4

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20:

GCTGCCACCC AGACCATATG TGGCTGCTCC T 31

(2) INFORMATION FOR SEQ ID NO: 21:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 30 BASE PAIRS
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: LINEAR

(ix) FEATURE:
(D) OTHER INFORMATION: OLIGOMER C21-1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:

GATGATGCTG CAGGTAAGCA GAGAGAATTC 30

(2) INFORMATION FOR SEQ ID NO: 22:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 BASE PAIRS
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: LINEAR

(ix) FEATURE:
(D) OTHER INFORMATION: OLIGOMER C21-2

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22:

AAGCAGAGAG AATTC 15

(2) INFORMATION FOR SEQ ID NO: 23:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 36 BASE PAIRS
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR
- (ix) FEATURE:
 - (D) OTHER INFORMATION: OLIGOMER C21-3
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23:

CTTCCACCGG CCCGATAGCA GGTGAGCGCC ACTGAG 36

(2) INFORMATION FOR SEQ ID NO: 24:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 36 BASE PAIRS
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR
- (ix) FEATURE:
 - (D) OTHER INFORMATION: OLIGOMER C21-4
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24:

CTCACTGATA TCCATATGGT CCTCGCAGGG CTGCTG 36

(2) INFORMATION FOR SEQ ID NO: 25:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 27 BASE PAIRS
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR
- (ix) FEATURE:
 - (D) OTHER INFORMATION: OLIGOMER C21-5
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 25:

AGCTCAGAAT TCCTTCTGGA TGGTCAC

27

(2) INFORMATION FOR SEQ ID NO: 26:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 12 BASE PAIRS
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: UNKNOWN

- (ix) FEATURE:
(D) OTHER INFORMATION: FIGURE 29,
pGBC21-2

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 26:

CCAGCCATGG TC

12

(2) INFORMATION FOR SEQ ID NO: 27:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 9 BASE PAIRS
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: UNKNOWN

- (ix) FEATURE:
(D) OTHER INFORMATION: FIGURE 29,
pGBC21-2

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 27:

AAGGAATTC

9

(2) INFORMATION FOR SEQ ID NO: 28:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 BASE PAIRS
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: LINEAR

(ix) FEATURE:
(D) OTHER INFORMATION: OLIGOMER C21-4

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 28:

CTCACTGATA TCCATATGGT C

21

(2) INFORMATION FOR SEQ ID NO: 29:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 BASE PAIRS
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: LINEAR

(ix) FEATURE:
(D) OTHER INFORMATION: OLIGOMER C21-5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 29:

AAGGAATTCT GAGCT

15

(2) INFORMATION FOR SEQ ID NO: 30:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 36 BASE PAIRS
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: LINEAR

(ix) FEATURE:
(D) OTHER INFORMATION: OLIGOMER C21-6

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 30:

CCTCTGCCTG GGTCGACAAA AATGGTCCTC GCAGGG

36

(2) INFORMATION FOR SEQ ID NO: 31:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 36 BASE PAIRS

- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: UNKNOWN

- (ix) FEATURE:
 - (D) OTHER INFORMATION: PGBC21-2,
FIGURE 33

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 31:

CCTCTGCCTG GGTCTCCAGC CATGGTCCTC GCAGGG

36

- (2) INFORMATION FOR SEQ ID NO: 32:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 18 BASE PAIRS
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR

- (ix) FEATURE:
 - (D) OTHER INFORMATION: OLIGOMER 11 BETA-1

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 32:

GGCAGTGTGC TGACACGA

18

- (2) INFORMATION FOR SEQ ID NO: 33:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 30 BASE PAIRS
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR

- (ix) FEATURE:
 - (D) OTHER INFORMATION: OLIGOMER 11 BETA-2

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 33:

CCGCACCCTG GCCTTTGCCC ACAGTGCCAT

30

(2) INFORMATION FOR SEQ ID NO: 34:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 36 BASE PAIRS
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: LINEAR

(ix) FEATURE:
(D) OTHER INFORMATION: OLIGOMER 11 BETA-3

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 34:

CAGCTCAAAG AGAGTCATCA GCAAGGGGAA GGCTGT 36

(2) INFORMATION FOR SEQ ID NO: 35:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 42 BASE PAIRS
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: LINEAR

(ix) FEATURE:
(D) OTHER INFORMATION: OLIGOMER 11 BETA-4

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 35:

TTTGATATCG AATTCCATAT GGGCACCAGA GGTGCTGCAG CC 42

(2) INFORMATION FOR SEQ ID NO: 36:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 42 BASE PAIRS
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: LINEAR

(ix) FEATURE:
(D) OTHER INFORMATION: OLIGOMER 11 BETA-5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 36:

TAACGATATC CTCGAGGGTA CCTACTGGAT GGCCCGGAAG GT

42

(2) INFORMATION FOR SEQ ID NO: 37:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 39 BASE PAIRS
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: LINEAR

- (ix) FEATURE:
(D) OTHER INFORMATION: OLIGOMER 11 BETA-6

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 37:

CTTCAGTCGA CAAAATGGG CACCAGAGGT GCTGCAGCC

39

(2) INFORMATION FOR SEQ ID NO: 38:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 BASE PAIRS
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: UNKNOWN

- (ix) FEATURE:
(D) OTHER INFORMATION: REGION IN 11 BETA
cDNA HOMOLOGOUS TO PRIMERS, FIGURE 36

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 38:

CGCCTACTGG GCACCAGA

18

(2) INFORMATION FOR SEQ ID NO: 39:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 BASE PAIRS
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: UNKNOWN

- (ix) FEATURE:
(D) OTHER INFORMATION: REGION IN 11 BETA
cDNA HOMOLOGOUS TO PRIMERS, FIGURE 36

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 39:

GCCATCCAGT AGTCGTGTCA G 21

- (2) INFORMATION FOR SEQ ID NO: 40:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 30 BASE PAIRS
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: LINEAR

- (ix) FEATURE:
(D) OTHER INFORMATION: OLIGOMER 11 BETA-4,
FIGURE 36

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 40:

TTTGATATCG AATTCCATAT GGGCACCAGA 30

- (2) INFORMATION FOR SEQ ID NO: 41:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 33 BASE PAIRS
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: LINEAR

- (ix) FEATURE:
(D) OTHER INFORMATION: OLIGOMER 11 BETA-5,
FIGURE 36

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 41:

GCCATCCAGT AGGTACCCTC GAGGATATCG TTA 33

- (2) INFORMATION FOR SEQ ID NO: 42:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 27 BASE PAIRS
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: UNKNOWN
- (ix) FEATURE:
 - (D) OTHER INFORMATION: OLIGOMER 11 BETA-6,
FIGURE 37
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 42:

CTTCAGTCGA CAAAAATGGG CACCAGA

27

(2) INFORMATION FOR SEQ ID NO: 43:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 39 BASE PAIRS
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR
- (ix) FEATURE:
 - (D) OTHER INFORMATION: OLIGOMER ADX-1
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 43:

CTTCAGTCGA CAAAAATGAG CAGCTCAGAA GATAAAATA

39

(2) INFORMATION FOR SEQ ID NO: 44:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 40 BASE PAIRS
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR
- (ix) FEATURE:
 - (D) OTHER INFORMATION: OLIGOMER ADX-2
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 44:

TGTAAGGTAC CCGGGATCCT TATTCTATCT TTGAGGAGTT

40

(2) INFORMATION FOR SEQ ID NO: 45:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 BASE PAIRS
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: UNKNOWN

(ix) FEATURE:
(D) OTHER INFORMATION: REGION OF ADX
mRNA/cDNA HOMOLOGOUS TO THE PRIMERS,
FIGURE 38

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 45:

CGAGCGCAGA GCAGCTCA

18

(2) INFORMATION FOR SEQ ID NO: 46:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 BASE PAIRS
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: UNKNOWN

(ix) FEATURE:
(D) OTHER INFORMATION: REGION OF ADX
mRNA/cDNA HOMOLOGOUS TO THE PRIMERS,
FIGURE 38

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 46:

ATAGAATAAA TAGGAATA

18

(2) INFORMATION FOR SEQ ID NO: 47:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 27 BASE PAIRS
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: LINEAR

(ix) FEATURE:
(D) OTHER INFORMATION: OLIGOMER ADX-1,
FIGURE 38

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 47:

CTTCAGTCGA CAAAAATGAG CAGCTCA 27

(2) INFORMATION FOR SEQ ID NO: 48:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 28 BASE PAIRS
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: LINEAR

(ix) FEATURE:
(D) OTHER INFORMATION: OLIGOMER ADX-2,
FIGURE 38

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 48:

ATAGAATAAG GATCCCGGGT ACCTTACA 28

(2) INFORMATION FOR SEQ ID NO: 49:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 BASE PAIRS
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: LINEAR

(ix) FEATURE:
(D) OTHER INFORMATION: OLIGOMER ADR-1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 49:

GGCTGGGATC TAGGC 15

(2) INFORMATION FOR SEQ ID NO: 50:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 36 BASE PAIRS
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: LINEAR
- (ix) FEATURE:
(D) OTHER INFORMATION: OLIGOMER ADR-2
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 50:

CACCACACAG ATCTGGGGGG TCTGCTCCTG TGGGGA 36

(2) INFORMATION FOR SEQ ID NO: 51:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 36 BASE PAIRS
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: LINEAR
- (ix) FEATURE:
(D) OTHER INFORMATION: OLIGOMER ADR-3
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 51:

TTCCATCAGC CGCTTCCTCG GCGAGCGGC CTCCT 36

(2) INFORMATION FOR SEQ ID NO: 52:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 36
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: LINEAR
- (ix) FEATURE:
(D) OTHER INFORMATION: OLIGOMER ADR-4
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 52:

CGAGTGTCGA CAAAATGTC CACACAGGAG CAGACC 36

(2) INFORMATION FOR SEQ ID NO: 53:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 36 BASE PAIRS
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: SINGLE

(D) TOPOLOGY: LINEAR

- (ix) FEATURE:
(D) OTHER INFORMATION: OLIGOMER ADR-5

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 53:

CGTGCTCGAG GTACCTCAGT GCCCCAGCAG CCGCAG 36

(2) INFORMATION FOR SEQ ID NO: 54:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 BASE PAIRS
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: LINEAR

- (ix) FEATURE:
(D) OTHER INFORMATION: SYNTHETIC OLIGOMER
USED TO SCREEN BOVINE ADRENAL CORTEX
cDNA LIBRARY

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 54:

TGCCAGTTCG TAGAGCACAT TGGTGCGTGG CGGGTTAGTG 40

ATGTCCAGGT 50

(2) INFORMATION FOR SEQ ID NO: 55:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 BASE PAIRS
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE

(D) TOPOLOGY: UNKNOWN

(ix) FEATURE:

(D) OTHER INFORMATION: REGION OF ADR cDNA
HOMOLOGOUS TO PRIMERS, FIGURE 40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 55:

CAGCACTTCT CCACACAG

18

(2) INFORMATION FOR SEQ ID NO: 56:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 18 BASE PAIRS
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: UNKNOWN

(ix) FEATURE:

(D) OTHER INFORMATION: REGION OF ADR cDNA
HOMOLOGOUS TO PRIMERS, FIGURE 40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 56:

GGGCACTGAG CCTAGATC

18

(2) INFORMATION FOR SEQ ID NO: 57:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 27 BASE PAIRS
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: LINEAR

(ix) FEATURE:

(D) OTHER INFORMATION: PRIMER ADR4,
FIGURE 40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 57:

CGAGTGTCGA CAAAAATGTC CACACAG

27

(2) INFORMATION FOR SEQ ID NO: 58:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 BASE PAIRS
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: LINEAR

- (ix) FEATURE:
(D) OTHER INFORMATION: PRIMER ADR5,
FIGURE 40

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 58:

GGGCACTGAG GTACCTCGAG CACG

24

(2) INFORMATION FOR SEQ ID NO: 59:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 BASE PAIRS
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: LINEAR

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 59:

GCGCTCAGCG GCCGCTTTCC AGTCG

25

(2) INFORMATION FOR SEQ ID NO: 60:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 BASE PAIRS
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: LINEAR

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 60:

AATTGCGGCC GCGTACGTAT G

21

(2) INFORMATION FOR SEQ ID NO: 61:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 BASE PAIRS
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: LINEAR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 61:

AATTCATACG TACGCGGCCG C 21

(2) INFORMATION FOR SEQ ID NO: 62:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 55 BASE PAIRS
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: LINEAR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 62:

GAATTCATAC GTACGCGGCC GCAATTGCGG CCGGTACGTA 40

TAATTCACTG GCCGT 55

(2) INFORMATION FOR SEQ ID NO: 63:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 14 BASE PAIRS
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: LINEAR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 63:

CAACGCGTCC TAGG 14

(2) INFORMATION FOR SEQ ID NO: 64:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 BASE PAIRS
(B) TYPE: NUCLEIC ACID

(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: LINEAR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 64:

AATTCCTAGG ACGCGTTGAG CT

22

(2) INFORMATION FOR SEQ ID NO: 65:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 33 BASE PAIRS
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: LINEAR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 65:

GATCCGCAGA TATCATCTAG ATCCCGGGTA GAT

33

(2) INFORMATION FOR SEQ ID NO: 66:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 39 BASE PAIRS
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: LINEAR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 66:

AGAGCTCAAG ATCTACCCGG GATCTAGATG ATATCTGCG

39

(2) INFORMATION FOR SEQ ID NO: 67:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 34 BASE PAIRS
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: LINEAR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 67:

CTTGAGCTCT ACGCAGCTGG TCGACACCTA GGAG

34

(2) INFORMATION FOR SEQ ID NO: 68:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 28 BASE PAIRS
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: LINEAR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 68:

AATTCTCCTA GGTGTCGACC AGCTGCGT 28

(2) INFORMATION FOR SEQ ID NO: 69:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 40 BASE PAIRS
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: LINEAR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 69:

GCGGATCTGC TCGAAGATTG CCTGCGCGTT GGGCTTGATC 40

(2) INFORMATION FOR SEQ ID NO: 70:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 BASE PAIRS
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: LINEAR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 70:

TCGACGGACG CGTGG 15

(2) INFORMATION FOR SEQ ID NO: 71:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 14 BASE PAIRS

- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: SINGLE
- (D) TOPOLOGY: LINEAR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 71:

TCGACCACGC GTCC

14

(2) INFORMATION FOR SEQ ID NO: 72:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 35 BASE PAIRS
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 72:

TGGCCGTCGT TTTACTCCTG CGCCTGATGC GGTAT

35

(2) INFORMATION FOR SEQ ID NO: 73:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 15 BASE PAIRS
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 73:

GGCCGCAAAA CAAA

15

(2) INFORMATION FOR SEQ ID NO: 74:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 15 BASE PAIRS
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 74:

AGCTTTTGGT TTTGC

15

(2) INFORMATION FOR SEQ ID NO: 75:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 BASE PAIRS
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 75:

GATCTATCGA TCGGCCCGCG

20

(2) INFORMATION FOR SEQ ID NO: 76:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 BASE PAIRS
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 76:

CGCGCGCGGC CGCATCGATA

20

(2) INFORMATION FOR SEQ ID NO: 77:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 14 BASE PAIRS
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 77:

AATTGGACGC GTCC

14

(2) INFORMATION FOR SEQ ID NO: 78:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 12 BASE PAIRS
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: LINEAR

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 78:

CACAAGCTTG TG

12

- (2) INFORMATION FOR SEQ ID NO: 79:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 12 BASE PAIRS
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: LINEAR

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 79:

TCGAGGGAAG CT

12

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